



Figure 1A

1 GGAAGTCAGCAGGGCGTTGGGGAGGGGAAATAGGGGGAGGCAGC
51 AGCCCCAGCCCTCAGAGAACAGCAGAAAGGGAGGGAGGGTGGCTGG
101 GGGACAGCCCCCACCATT CCTACCGCTATGGCCCAAACCTCCCCACTCC
151 CACCTCCCCTCCATCGGCCGGCTAGGACACCCCCAAATCCCGTGGCC
201 CCTTGGCACCGACACCCCCGACAGAGACAGAGACACAGAGACACAG
251 CCGCTGCCGCAGCAGGGCTGGCTGGGGAGGGCCAGCCCCAGCCCCCTAC
301 CCCTCTGAGGTGGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTC CTC C
Met Leu Leu Leu Leu Phe Leu Leu Leu Phe L
10
20
380 TG CTG CCC ACC CTC TGG TTC AGC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys
30

Replacement Sheet
Appl. No.: 10/667,494
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Atty. Docket No.: 077319-0381

Figure 1B

418 TAC TTC TAC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA CGC CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

80

Figure 1C

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G
90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
Iln Pro Tyr Val Val Ser Asn His Gln Ser Ser Leu
100.

643 GAT CTG CTT GGG ATG ATG GAG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C
110

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly
130

Figure 1D

718 TCT GCC GGG CTG GCC TGC TGG CTC GCA GGA GTC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P

140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val

150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V

160

170

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His

180

Figure 1E

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H

190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile

200

943 GTC ATG TCC TCC TAC CAA GAC TAC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G

210

220

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val

230

Figure 1F

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A

240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met

250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G

260

1130 GT GGT GGT GAC TAT CTG AAG CCT GGG GGC GGT GGG
1y Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCCATCTGTCCCCATCTTCCTCCCC

1216 CACACCTACCCACCCAGGGCCCTGAAGCAGGGCAAACCCCTCTTCCTT

1266 GtCTCCCTCTCCCTTATTCTCCACTTGAATCTCAACTTCTTGAA

Figure 1G

1316 GTGAATGTGGATAACAGGCCACTCGGTGCAGTTCCACTCTGCCCTCTGGCCCCATCCATTGG
1366 ACTCTTGCCTCGGTGCAGTTCCACTCTGCCCTCTGGCTTGCCTCCTCATCTCCCTCATCAGTCAGCCTACAC
1416 TGTCTGTGGACAGTTGCCTCCTCATCTCCCTCATCAGTCAGTGGAGTCTTCCTATGTGGTCTT
1466 AAGGGAGGGAAACATTTCCATCCCCCACATGGCCAGTGGACTCATCCATTCTTGGA
1516 CTCTACCCCTCTACCCCCACATGGGATTCAATGGACTCATCCATT
1566 ACAAATCCCCCCCCTCAAAAGTCCATGGATTCAATGGACTCATCCATT
1616 TGTGAGGGAGCTTCTGCCCTCTGGCTGAAGCTGATACCTGAAAGCACT
1666 CCCAGGGCTCATCCTGGAGCTTFCCTCAGCACCTCACCTTCCCTCCAG
1716 TGTAGCCCTCCTGTCAAGTGGGGCTGGACCCCTTCTAATTCAAGGGTCTCAT
1766 GCCTGCCCTTGCCCAAGATGCCAGGGTCACTCTGGGATAACCACT
1816 TCAGTCTCCACATTCTGGTTCTGTCCCCATAGTACAGTTCTCAGTG
1866 GACATGCCCAACCCAGCCCCCTGGCAGCCCCCTGCTGACCACATCTCACCAGAC
1916 ACAAGGGAAAGCAGACATCAGGTGCTGCACTCACTTCTGCCCTGG
1966 GGAGTTGGGAAAGGAACGAACCCCTGGCTGGAGGGATAAGGAGGGCTTTT

Figure 1H.

2016 AATTTATTTCCTTTCTGTGGCTTCCCCCTCTGAGCCAGTTTCA
2066 TTtCTTCCCTGGCATTAGCCACTCCCTGCCTCTCACTCCAGACCTGTT
2116 CCCACAACTGGGGAGGTAGGCTGGAGCAAAGGAGGGTGGACCCAG
2166 TTTTGCCTGGTTTTATTATAATTATCTGGATAACAGCAAAAAACTG
2216 AAAATAAAGAGAGAGAAAAAAA

Figure 2 A

	10	20	30	40	50
Human LPAAT	1 <u>MDLWPGAWM-</u>	----- <u>LLLLLF</u>	<u>LL-LLFLLPT</u>	<u>LWFCSPSAKY</u>	<u>E-----FKMA</u>
Yeast LPAAT	1 <u>MSV-IGRFLY</u>	<u>YLRSVL-VVL</u>	<u>AL-AG-----</u>	<u>C-----C</u>	<u>G-----G</u>
E. coli LPAAT	1 <u>M-----</u>	<u>-----LYIF</u>	<u>RL-ITIVIYS</u>	<u>ILVCVFGSIY</u>	<u>-----</u>
Maize LPAAT	1 <u>MAI-----</u>	<u>---PLVLVVL</u>	<u>PLGLLELLSG</u>	<u>LIVNAIQAVL</u>	<u>FVTIRFESKS</u>
	60	70	80	90	100
Human LPAAT	51 <u>FYNGWILFLA</u>	<u>VLAIPVCAVR</u>	<u>GRNVENNMKIL</u>	<u>RMLLHIIKYL</u>	<u>-YGIRIVEVRG</u>
Yeast LPAAT	51 <u>FY-----G</u>	<u>VIAISILCTLI</u>	<u>GKQHLAQWIT</u>	<u>MLGLDV---K</u>	<u>-----</u>
E. coli LPAAT	51 <u>-----</u>	<u>-----CLFS</u>	<u>PRNPKHVATF</u>	<u>GHMFGRLLAPL</u>	<u>-FGLKVECRK</u>
Maize LPAAT	51 <u>FYRRINRFLA</u>	<u>EL-----</u>	<u>-----L</u>	<u>WLQLWVWVVDW</u>	<u>WAGVVKVQLHA</u>
	110	120	130	140	150
Human LPAAT	101 AHHF-PPSQ-	-PYVVVSNNHQ	<u>SSLDL LGMME</u>	<u>VL-----</u>	<u>-PGRC--</u>
Yeast LPAAT	101 VVGE-ENLAK	<u>KPYIMIANHQ</u>	<u>STLDIFMLGR</u>	<u>IF-----</u>	<u>-PPGCT-</u>
E. coli LPAAT	101 PTDA-ESYG-	<u>-NAYIYIANHQ</u>	<u>NNYDMVTAQN</u>	<u>IVQ-PP-----</u>	<u>TIVV-GKKSL</u>
Maize LPAAT	101 DEETYRSMGK	<u>EHALLISNHR</u>	<u>SDIDWL-IGW</u>	<u>LLAQRSGGCLG</u>	<u>STLAVMKKSS</u>
	160	170	180	190	200
Human LPAAT	151 <u>LWAGSAGLAC</u>	<u>W---LAGVIF</u>	<u>IDRKRTGDAI</u>	<u>SVMSEVAQTL</u>	<u>LTQDVRVWV-</u>
Yeast LPAAT	151 <u>KYVPEFLG</u>	<u>-----</u>	<u>LDRSKRQEAI</u>	<u>DTLNKGLENV</u>	<u>KKNKRALWV-</u>
E. coli LPAAT	151 <u>LWIPFFGQLY</u>	<u>W---LTGNLL</u>	<u>IDRNNRTKAH</u>	<u>GTIAEVVNHF</u>	<u>KKRRISIWM-</u>
Maize LPAAT	151 <u>KFLPVIGWSM</u>	<u>WF---AEYLF</u>	<u>LERS-WAKDE</u>	<u>KTLKWGLQRL</u>	<u>KDFPRPFWLA</u>
	210	220	230	240	250
Human LPAAT	201 <u>-FPEGTRNHN</u>	<u>GS-----</u>	<u>-----</u>	<u>MLPFKRGAFH</u>	<u>LAVQAQVPIV</u>
Yeast LPAAT	201 <u>-FPEGTRSYT</u>	<u>SEL-----</u>	<u>-----T</u>	<u>MLPFKKGAFH</u>	<u>LAQQGKIPIV</u>
E. coli LPAAT	201 <u>-FPEGTRSRC</u>	<u>RGL-----</u>	<u>-----</u>	<u>-LPFKTGAFH</u>	<u>AIAAGVPII</u>
Maize LPAAT	201 <u>LFVEGTRFTP</u>	<u>AKLLAAQEYA</u>	<u>ASQGLPAPRN</u>	<u>VLIPIRTKGCFV</u>	<u>SAVSIMRDFV</u>

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Figure 2 B

Human LPAAT	251	<u>PIVMSSYQDF</u>	<u>YCKKERRFTS</u>	<u>GOCQVRVLPP</u>	<u>VPTEGLTPDD</u>	<u>VPALADR</u>	260	270	280	290	300
Yeast LPAAT	251	<u>PVWVSNTSTL</u>	<u>VSPKIGVFNRL</u>	<u>GCMIVRILKP</u>	<u>ISTENLTKDK</u>	<u>IGEFAEK</u>					
E. coli LPAAT	251	<u>PVCVSTTSNK</u>	<u>I--NLNRHLHN</u>	<u>GLVIVEMLPP</u>	<u>IDVSQYGKDQ</u>	<u>VRELAAH</u>					
Maize LPAAT	251	<u>PAIYDITT--V</u>	<u>IVPKDSPQPT</u>	<u>MRLILKGQSS</u>	<u>VIHVRMKRHA</u>	<u>MSEMPKSDED</u>					
Human LPAAT	301	-----	<u>VRHSMMLTV-F</u>	<u>REISTTDGRGG</u>	<u>GDYLKKPGGG</u>	<u>G*</u>	310	320	330	340	350
Yeast LPAAT	301	-----	<u>VRDQMVDT-L</u>	<u>KEIGYSPAIN</u>	<u>DTLPPQ</u>	-----					
E. coli LPAAT	301	-----	<u>CRSIMEQK-I</u>	<u>AELDKEVAE</u>	-----	<u>REAGK V*</u>					
Maize LPAAT	301	VSKWCKDIFV	<u>AKDALLDKHL</u>	<u>ATGTFDEEIR</u>	<u>PIGRPVVKSLL</u>	<u>VTLFWSCLL</u>	360	370	380	390	400
Human LPAAT	351	-----	-----	-----	-----	-----					
Yeast LPAAT	351	<u>-AIEY---A</u>	<u>AL</u>	<u>Q</u>	<u>HDKKVNNKKIK</u>	<u>NEPVPSVSIS</u>	<u>NDVNTHNEG_S</u>				
E. coli LPAAT	351	-----	-----	-----	-----	-----	-----				
Maize LPAAT	351	<u>FGAIEFFFKWT</u>	<u>QLLSTWRGVA</u>	<u>FTAAGMALVT</u>	<u>GVMHVFIMFS</u>	<u>QA</u>	<u>--ERS</u>				
Human LPAAT	401	-----	-----	-----	-----	-----					
Yeast LPAAT	401	<u>S</u>	<u>--V</u>	<u>KKMH*</u>	-----	-----					
E. coli LPAAT	401	-----	-----	-----	-----	-----					
Maize LPAAT	401	<u>SSARAARNRV</u>	<u>KKE*</u>	-----	-----	-----					
		410	420	430	440	450					

Figure 3 A

10	20	30	40	50	60
GGAGCGAGCT	GGCGGCCG	TGGGGCCG	GGCGGCCA	TGGAGCTGTG	GCGTGTCTG
70	80	90	100	110	120
GCGCGGCC	TGCTGTTGCT	GCTGCTGCTG	GTGCAGCTGA	GCGCGCCGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAGGTCTG	CCCTGTACTG	CGCGCTGTGC	TTCACGGTGT	CCGCCTGGC	CTCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGGG	CGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGGC	CAGGCTCTGCA
310	320	330	340	350	360
GAGGCCGTC	CCTGTGTCA	CGTCTCCAAC	CACCAAGAGCA	TCCTGGACAT	GATGGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TTCCGGAGCG	CTGGCGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGC	GTCTTCTTCA	TCACCGGCA	GGGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACTCTGGC	GAGCGCATGG	TCAGGGAGAA	CCTCAAAGTG

Figure 3 B

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGAAACGAC	AATGGGGACC	TGCTGCCTTT	TAAGAAGGGC
610	620	630	640	650	660
GCCTTCTTAC	TGGCACTCCA	GGCACACAGGTG	CCCATCGTCC	CCGTGGTGT	CTCTTCCTTC
670	680	690	700	710	720
TCCTCCTTCT	ACAAACACCAA	GAAGGAAGTTTC	TTCACTTCAG	GAACAGTCAC	AGTGCAGGGTG
730	740	750	760	770	780
CTGGAAGCCA	TCCCCCACCAG	CGGCCTCACT	GCGGGGGACG	TCCCCTGGCCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCCGGG	CCATGAGGAC	CACCTTCCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGGGGGCC	CAGTAGCCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGCA	GAGGGGACTC	CTCCCGGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCGGGAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGGCCCT	GGTGTCCCT	GCAGGGGGCT	CAGCTGGACC

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Replacement Sheet

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ACYLTRANSFERASE GAMMA-1

POLYPEPTIDE (As Amended)

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Figure 3C

1090	1100	1110	1120	1130	1140
CTCCCCGGGC	TCGAGGGCAG	GGACTCGGCC	CCACGGCAC	TCTGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCGCTGGT	GGGCTGAGCC	ACAAGGCC	CGATGGCCA
1210	1220	1230	1240	1250	1260
GGAGGAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCCAGACT	CACGCCACCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGAA	TCGGGGCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGG	GTCAAGCACTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTT	ATAAACACAC	TCTTGAAAAA	AAAAAAA	AAAAAAA
1390	1400	1410	1420	1430	1440
AAA.....

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Figure 4 A

10 20 30 40 50
GGAGCGAGGCTGGCGGCCGTGGCCGGGGCC ATG GAG CTC TCG CCG
Met Glu Leu Trp Pro

60 70 80 90
TGT CTG GCC GCG GCG CTC CTC CTG TTG CTC CTC CTG GTG CAG CTG
Cys Leu Ala Ala Ala Leu Leu Leu Leu Val Gln Leu

10 20
10 110 120 130 140
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC CTC TGC TGC GCG
Ser Arg Ala Ala Glu Phe Tyr Ala Lys Val Ala Leu Tyr Cys Ala

150 160 170 180
CTG TTC ACG GTG TCC GCC GTG GCC TCG CTC GTC TGC TGC CTG CTG
Leu Cys Phe Thr Val Ser Ala Val Ala Ser Leu Val Cys Leu Leu

40 50
190 200 210 220 230
TGC CAC GGC GGC CGG ACC GTG GAG AAC ATG AGC ATC ATC GGC TGG
Cys His Gly Gly Arg Thr Val Glu Asn Met Ser Ile Ile Gly Trp

60

Figure 4B

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Figure 4C

510	CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT	520	Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr	530	160
550	CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CCT CCT TTT AAG	560	Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys	570	170
600	AAG GCC TTC TAC CTG GCA GTC CAG GCA CAG GTC CCC ATC GTC	610	Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val	620	180
640	CCC GTG GTG TAC TCT TCC TTC TCC TAC AAC ACC AAG AAG	650	Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys	660	190
690	AAG TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC	700	Lys Phe Phe Thr Ser Gly Thr Val Val Thr Val Gln Val Leu Glu Ala	710	220
720	730	230			

Figure 4 D

730 740 750 760 770
ATC CCC ACC AGC GGC CTC ACT GCG GCG GAC GTC CCT GCG CTC GTG
Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val
240

780 790 800 810 820
GAC ACC TGC CAC CGG GCC ATG AGG ACC ACC TTC CTC CAC ATC TCC
Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe Leu His Ile Ser
250

830 840 850 860
AAG ACC CCC CAG GAC AAC GGG GCC ACT GCG GGG TCT GGC GTG CAG
Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln
270

870 880 890 900 910 920
CCG GCC CAG TAG CCCAGACCACGGCAGGGCATGACCTGGGAGGGCAGGTGGAAGC
Pro Ala Gln ***

940 950 960 970 980
CGATGGCTGGGGATGGGCAGAGGGGACTCCTCCGGCTTCCAAATAACCACTCTGTCCGG
990 1000 1010 1020 1030 1040
CTCCCCCAGCTCACTCTAGCCCCGGAAAGCCAGGGAAAGCCCTTCTGTCACTGGTCTCAGAC
1050 1060 1070 1080 1090 1100
ACAGGGCCCTGGTGTCCCCCTGAGGGGCTCAGCTGGACCCCTGGGGCTCGAGGGCAG

Figure 4 E

Replacement Sheet

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1110	1120	1130	1140	1150	1160	
	GGACTCGGCCACGGCACCTCTGGGNNGCTGGGNTGATAAGATGAGGCTTGGCTGTG					
1170	1180	1190	1200	1210	1220	
	GCCCGCTGGCTGAGGCCACAAGGCCCCGATGGCCAGGAGATGGGAGGACCCC					
1230	1240	1250	1260	1270	1280	
	GAGGCCAGGAGTCCCCAGACTCACGCACCCCTGGGCCACAGGGAGCCGAATCGGGCCTG					
1290	1310	1320	1330	1340		
	CTGGCTCCCTGGCTGAAGAATCTGTGGGTCAAGCACTGTACTCCGTTGCTGTAAAAAA					
1350	1360	1370	1380			
	ATAAACACACTCTTGGAAAAAAA					

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Alignment of LPAAT Sequences.

	10	20	30	40	50	
Human LPAAT- β	-----	-----	-----	MEL WPC-----LA A <u>L</u> L <u>L</u> L <u>L</u> L <u>L</u> V		
Human LPAAT- α	1-----	-----	-----	MDL WPGAW <u>M</u> LL <u>L</u> L <u>L</u> FLLP		
Yeast LPAAT	1-----	-----	-----	MSV --IGRFLYYL RSV <u>L</u> W <u>L</u> ALA		
E. coli LPAAT	1-----	-----	-----	-----		
H. influenzae	1-----	-----	-----	-----		
S. typhimurium	1-----	-----	-----	-----		
L. douglassi	1 <u>M</u> A <u>K</u> T <u>R</u> <u>I</u> <u>S</u> -L <u>R</u> N <u>R</u> -----R <u>Q</u> L <u>K</u> P A <u>V</u> A <u>A</u> T <u>A</u> D--D DK <u>D</u> G <u>F</u> M <u>V</u> --					
C. nucifera	1 <u>M</u> D <u>A</u> <u>S</u> <u>G</u> <u>A</u> <u>S</u> <u>S</u> <u>F</u> -----R <u>G</u> R <u>C</u> E <u>S</u> <u>E</u> <u>K</u> A <u>S</u> <u>F</u> G <u>M</u> <u>S</u> <u>Q</u> <u>K</u> D A <u>A</u> G <u>Q</u> R <u>S</u> R <u>R</u> P <u>A</u> -----D <u>A</u> D <u>D</u> F <u>E</u> F <u>V</u> D <u>D</u>					
	60	70	80	90	100	
Human LPAAT- β	51 Q <u>L</u> ---S <u>R</u> A <u>E</u> F <u>Y</u> A <u>K</u> V <u>A</u> L <u>Y</u> C A <u>L</u> C <u>F</u> T <u>V</u> S <u>A</u> V <u>A</u> S <u>L</u> V <u>C</u> I <u>L</u> L <u>O</u> H <u>G</u> G R <u>T</u> V <u>E</u> N <u>M</u> -S <u>I</u> I					
Human LPAAT- α	51 T <u>I</u> W <u>F</u> C <u>S</u> <u>R</u> <u>A</u> K Y <u>F</u> F <u>K</u> M <u>A</u> F-Y <u>N</u> G <u>W</u> I <u>I</u> F <u>A</u> V <u>I</u> A <u>L</u> A IP <u>V</u> C <u>A</u> V--RG R <u>N</u> V <u>E</u> N <u>M</u> -K <u>I</u> L					
Yeast LPAAT	51 G---C <u>G</u> ---F <u>Y</u> ---S <u>I</u> L <u>C</u> I <u>L</u> I <u>C</u> Q H <u>I</u> A <u>Q</u> W <u>I</u> -T <u>A</u> R					
E. coli LPAAT	51 M <u>L</u> Y <u>I</u> F <u>R</u> I <u>I</u> T <u>V</u> I <u>S</u> I <u>L</u> V <u>C</u> ---V <u>F</u> G S <u>T</u> I <u>C</u> L <u>F</u> S <u>P</u> R <u>N</u> P <u>K</u> H <u>V</u> ---A <u>T</u> E					
H. influenzae	51 M <u>L</u> K <u>L</u> I <u>R</u> F <u>M</u> I <u>L</u> I <u>C</u> ---V <u>L</u> G T <u>I</u> Y S <u>T</u> I <u>R</u> E <u>K</u> N P <u>S</u> N <u>V</u> ---G <u>I</u> V					
S. typhimurium	51 M <u>L</u> Y <u>I</u> F <u>R</u> I <u>I</u> T <u>V</u> I <u>S</u> I <u>L</u> V <u>C</u> ---V <u>F</u> G S <u>T</u> I <u>C</u> L <u>F</u> S <u>P</u> R <u>N</u> P <u>K</u> H <u>V</u> ---A <u>T</u> E					
L. douglassi	51 D <u>R</u> W <u>T</u> I <u>V</u> I <u>L</u> S <u>V</u> F <u>K</u> I <u>F</u> V <u>C</u> E <u>A</u> F <u>T</u> V <u>W</u> I <u>I</u> T <u>A</u> V <u>W</u> G L <u>I</u> M <u>W</u> I <u>L</u> L <u>P</u> W <u>P</u> W <u>R</u> I <u>R</u> B <u>G</u> N <u>Y</u>					
C. nucifera	51 S <u>M</u> V <u>T</u> I <u>T</u> V <u>W</u> N M <u>I</u> M <u>I</u> L <u>I</u> P <u>P</u> W <u>P</u> Y <u>A</u> R <u>J</u> R <u>Q</u> G <u>N</u> Y					

Figure 5 B

Replacement Sheet
Appl. No.: 10/667,494
**Title: HUMAN LYSOPHOSPHATIDIC ACID
ACYLTRANSFERASE GAMMA-1
POLYPEPTIDE (As Amended)
Inventors: David W. LEUNG et al.
Atty. Docket No.: 077319-0381**

Human LPAAT- β	101 <u>GWFVRSFKY</u> -- <u>FYGLRFEV</u> RDPRRLQEAR PCV <u>IVSNHQ</u> S ILDM <u>YGMIEV</u>	110	120	130	140	150
Human LPAAT- α	101 RLM <u>IHIKY</u> --LYG <u>IRVEV</u> RGAHHFPPSQ PYV <u>VSNHQ</u> S SLD <u>LGMMEV</u>					
Yeast LPAAT	101 CFY-HM <u>MKL</u> --ML <u>GLDDMKV</u> VGE <u>ENNAK-K</u> PYIM <u>LANHQ</u> S TLD <u>IFMLGR</u> I					
E. coli LPAAT	101 GHMF <u>GRL</u> -- APL <u>FGLIKVEC</u> RKE <u>PTDAE</u> SYG NAI <u>YIANTHQN</u> NYDM <u>VTA</u> SN					
H. influenzae	101 ARW <u>FGRL</u> -FT Y <u>PLFGLKVEH</u> R <u>PQDQKQIS</u> RAI <u>YIGNHQN</u> NYDM <u>VTA</u> NI					
S. typhimurium	101 GHMF <u>GRL</u> -FT APL <u>FGLIKVEC</u> R <u>KPADAENY</u> NAI <u>YIANTHQN</u> NYDM <u>VTA</u> NI					
L. douglassi	101 GH <u>ITCGIV</u> -- IWIY <u>GIPIKI</u> Q <u>GSEEHKKRA</u> IFTY <u>ISNHS</u> PI <u>DAFFVMM</u>					
C. nucifera	101 GH <u>ITCRM</u> ,FT MW <u>GNPITI</u> EG <u>SEFSNTRA</u> I--YI <u>ONHAS</u> IVD <u>FLIMM</u>					
Human LPAAT- β	160 RE <u>LLFLGPV</u> -- <u>GLIMYLGV</u> FE <u>INRQRSS</u> AMT--VM <u>AIL</u>	170	180	190	200	
Human LPAAT- α	151 LP <u>ERCVQLA</u> K RE <u>LLWAGSA</u> -- <u>GLACWLAGV</u> I <u>EDDRKR</u> CD A <u>IS</u> --VM <u>SEV</u>					
Yeast LPAAT	151 LP <u>GRCVPIA</u> K RE <u>LLWAGSA</u> -- <u>GLACWLAGV</u> I <u>EDDRKR</u> CD A <u>IS</u> --VM <u>SEV</u>					
E. coli LPAAT	151 FPP <u>GCTVTA</u> K KSL <u>KKVPEI</u> I--GFW <u>MAISGT</u> Y <u>FLDRSKRQE</u> A <u>ID</u> --T <u>LNG</u>					
H. influenzae	151 VQP <u>PTVVGK</u> KSL <u>LMWIPFF</u> --GOL <u>YWLTG</u> N II <u>IDRNMR</u> TK A <u>FG</u> --T <u>IAEV</u>					
S. typhimurium	151 VQP <u>PTVVGK</u> KSL <u>LMWIPFF</u> T <u>GOLYWLTG</u> N II <u>IDRNMR</u> AK A <u>HS</u> --T <u>IAAV</u>					
L. douglassi	151 API <u>GTIVGVA</u> K KE <u>VWYPLL</u> G Q--LY <u>TTAAH</u> I <u>RIDRSNPAA</u> A <u>IQSFTMKEA</u>					
C. nucifera	151 IP <u>KGTVTAK</u> KE <u>IIWYPLFG</u> Q <u>FTLYVLANH</u> QR <u>IDRSNPAA</u> A <u>IQSFTMKEA</u>					

Figure 5C

Human LPAT- β	201	GERMREN <u>LK</u> <u>VWIVYPEGTRN</u> <u>DNGDL</u> —LPF	KKGAFYL—A	VOAQVPTIVPV
Human LPAT- α	201	AQTLITQDVR <u>VWVFPEGTRN</u> <u>HNGSM</u> —LPF	KRGAFHL—A	VQAQVPTIVPI
Yeast LPAT	201	LENVKKNRA <u>LWVFPEGTRS</u> <u>YTSELYMILPF</u>	KKGAFHL—A	QQGKLPTIVPV
E. coli LPAT	201	VNHFKKRRI <u>S</u> <u>IWMFPEGTRS</u> <u>RGRGL</u> —LPF	KTGAF—HAA	IAAGVPIIPV
H. influenzae	201	<u>ARRINEDNL</u> S <u>IWMFPEGTRN</u> <u>RGRGL</u> —LPF	KTGAFTHAA	ISAGVPIIPV
S. typhimurium	201	VNHFKKRRI <u>S</u> <u>IWMFPEGTRS</u> <u>RGRGL</u> —LPF	KTGAFTHAA	IAAGVPIIPV
L. douglassi	201	<u>VRVITTEKNL</u> S <u>LDMFPEGTRS</u> <u>GDGRL</u> —LPF	KKGFVHL—A	LQSILPTIVPM
C. nucifera	201	<u>ARAWKKNLS</u> <u>LIFPEGTRS</u> <u>KTGRL</u> —LPF	KKGFTHFTIA	LQTRLPTIVPM
	210	220	230	240
	250			
Human LPAT- β	251	VISSRSS—F	YNTKKKFITS	GIIVTVQVLEFA
Human LPAT- α	251	VMSSYQD—F	YCKKERRFTS	QQQQVRLPP
Yeast LPAT	251	WVSNTI <u>S</u> —L	VSPKYGVENR	GOMIVRILKP
E. coli LPAT	251	<u>CVSTIS</u> ---	NKINLNRIHN	IISTENLTKDK
H. influenzae	251	<u>YCSSTH</u> ---	NKDNLNRWDN	IGEFAEKVRD
S. typhimurium	251	<u>CVSNIS</u> ---	GKVTCIMDP	TDVSGCYTKDN
L. douglassi	251	ILTGTHLAWF	GLVTIVEMLPP	VRELAAHCRF
C. nucifera	251	VLTGTHLAW-	TRKGIFRVRP	IDDDWTVKD
	260	270	280	290
	300			

Figure 5D

	310	320	330	340	350
Human LPAAT- β	<u>AMRTTIFHIS</u>	<u>KTPQENGATA</u>	<u>GSGVQPAQ*</u>	—	—
Human LPAAT- α	<u>SMLTVFREIS</u>	<u>T_DGRCGGDXL</u>	<u>KRP<u>GGGG*</u></u>	—	—
Yeast LPAAT	<u>QMVTIILKEIG</u>	<u>YSPA<u>INDTIL</u></u>	<u>PFQATEYYAL</u>	<u>QDKKKKKIKI</u>	<u>KNEPVSVSI</u>
E. coli LPAAT	<u>-SIME<u>QKIAE</u></u>	<u>LD<u>KEVA</u></u> — ER	<u>EA<u>AGKV*</u></u>	—	—
H. influenzae	<u>T<u>LMEKRIA</u></u>	<u>LD<u>EETIA</u></u> —	—	<u>K<u>GN*</u></u>	—
S. typhimurium	<u>T<u>ALME<u>QKIAE</u></u></u>	<u>LD<u>KEVA</u></u> — ER	<u>EA<u>TGKV*</u></u>	—	—
L. douglasii	<u>T<u>YVRNIPASQ</u></u>	<u>KPLGS</u> — T <u>NR</u>	— S-K*	—	—
C. nucifera	<u>T<u>ALYMDHLPE</u></u>	<u>S<u>QKPLIVSKGR</u></u>	<u>D<u>ASGRSN<u>S*</u></u></u>	—	—
	360	370	380	390	
Human LPAAT- β	—	—	—	—	—
Human LPAAT- α	—	—	—	—	—
Yeast LPAAT	<u>SNDVNTHNEG</u>	<u>SSVKRMH*</u>
E. coli LPAAT	—	—	—	—	—
H. influenzae	—	—	—	—	—
S. typhimurium	—	—	—	—	—
L. douglasii	—	—	—	—	—
C. nucifera	—	—	—	—	—

Figure 9 A

TCTATGAAACCAACATA	CATGGCGTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG	60
GGCAGGTGTCTGGCTTGCCACCCGGAAGCCCTGAGGGCAGCTGTTCCCCTGGCTCTGC		120
<u>TGACCTTGTGCCTTGGACGGCTGTCTCAGCGAGGGCCGTGCACCCGCTCTGAGCAGC</u>		180
GCC <u>ATG</u> GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC		225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His		
5 10		
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC		270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn		
15 20 25		
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG		315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln		
30 35 40		
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC		360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser		
45 50 55		
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA		405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr		
60 65 70		
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC		450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His		
75 80 85		
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT		495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys		
90 95 100		
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG		540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys		
105 110 115		
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG		585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp		
120 125 130		
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG		630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu		
135 140 145		
GAG GAC CGG' GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC		675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp		
150 155 160		
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC		720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg		
165 170 175		
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT		765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala		
180 185 190		
AAG GGG CTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG		810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys		
195 200 205		
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT		855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala		
210 215 220		
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC		900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser		
225 230 235		
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC		945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys		
240 245 250		
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA		990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu		
255 260 265		
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC		1035

Figure 9 B

Ala Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu			
270	275	280	
CAG GAG ATA TAT AAT CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT			1080
Gln Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe			
285	290	295	
AAG CCT GCC CGG AGG CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG			1125
Lys Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp			
300	305	310	
GCC ACC ATT CTC CTG TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC			1170
Ala Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val			
315	320	325	
TTT GCC AGC GGA TCA CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT			1215
Phe Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe			
330	335	340	
GTG GGA GCA GCT TCC TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT			1260
Val Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Val Thr			
345	350	355	
GAG ATA GAA AAA GGC TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA			1305
Glu Ile Glu Lys Gly Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys			
360	365	370	
AAG GAA TAA TTAATGGCTGTGACTGAACACACAGCGGCCCTGACGGTGGTATCCAGTT			1362
Lys Glu ***			
AACTCAAAACCAACACACAGAGTCAGGAAAAGACAATTAGAAACTATTTTCTTATTAA			1422
CTGGTGACTAATATTAACAAAACCTTGAGCCAAGAGTAAAGAATTAGAAGGCCCTGTCAGG			1482
TGAAGTCTTCAGCCTCCACAGCGCAGGGTCCCAGCATCTCCACGCGCGCCCGTGGGAGG			1542
TGGGTCCGGCCGGAGAGGCCTCCCGCGGACGCCGTCTCCAGAACCTCCGCTTCCAAGAG			1602
GGACCTTGGCTGCTTCTCCTAAACTTAGATCAAATTTAAAAAAAAAAAAAAA			1660

Figure 10 A

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCCTCAACTGCCGCCCTCGCC	61
TACTCACTCTGGAGCCT <u>AGC</u> ACAAA <u>ACTAGAAGC</u> AACCCAAAGCACCTGTCACTGGAGACT	121
AATTATGC <u>GGC</u> ACCCATACAGGGACCC <u>CTGT</u> GGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTTA <u>AGC</u> AAAAAGGAAGTATA <u>ACAACAAAGTCCATA</u> ACTGGTC <u>ATG</u> CTG	238
Met Leu	
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

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POLYPEPTIDE (As Amended)
Inventors: David W. LEUNG et al.
Atty. Docket No.: 077319-0381

Figure 10 B

260	265	270	
CCT CTC	CTG ATC CTG ACT TTC	TTG GGG TTT GTG GGA GCA GCT TCC	1093
Pro Leu	Leu Ile Leu Thr Phe	Leu Gly Phe Val Gly Ala Ala Ser	
275	280	285	
TTT GGA GTT CGC AGA CTG ATA	GGAA GTA ACT GAG ATA GAA AAA GGC	1138	
Phe Gly Val Arg Arg Leu Ile	Gly Val Thr Glu Ile Glu Lys Gly		
290	295	300	
TCC AGC TAC GGA AAC CAA GAG	TTT AAG AAA AAG GAA TAA TTAATGGC	1185	
Ser Ser Tyr Gly Asn Gln Glu	Phe Lys Lys Lys Glu ***		
305	310		
TGTGACTGAACACACCGCGGCCCTGACGGTGGTATCCAGTTAAC	CTCAAACCAACACACAG	1245	
AGTCAGGAAAAGACAATTAGAAACTATTTCTTATTAACTGGTGACTAATATTAACAA		1305	
AACTTGAGCCAAGAGTAAAGAATT	CAGAAGGCCCTGTCAGGTGAAGTCTTCAGCCTCCCAC	1365	
AGCGCAGGGTCCCAGCATCTCCACGCGGCCGTGGAGGTGGTCGGCCGGAGAGGCC		1425	
TCCCGGGACGCCGTCTCCAGAACCTCGCTTCCAAGAGGGACCTTGGCTGCTTC		1485	
TCCTTAAACTTAGATCAAATTAAAAA			1523

Figure 11A

TGAACCCAGCCGGCTCATCTCAGCTTCTGGTTCTAAGTCCATGTGCCAAAGGCTGCCAG	61
GAAGGAGACGCCCTCCTGAGTCCTGGATCTTCTCTGGAAATCTTGACTGTGGG	121
<u>TAGTATTATTC</u> <u>TAAGAGCGTCCACGCATC</u> ATG GAC CTC GCG GGA CTG	175
Met Asp Leu Ala Gly Leu	
5	
CTG AAG TCT CAG TTC CTG TGC CAC CTG GTC TTC TGC TAC GTC TTT	220
Leu Lys Ser Gln Phe Leu Cys His Leu Val Phe Cys Tyr Val Phe	
10 15 20	
ATT GCC TCA GGG CTA ATC ATC AAC ACC ATT CAG CTC TTC ACT CTC	265
Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln Leu Phe Thr Leu	
25 30 35	
CTC CTC TGG CCC ATT AAC AAG CAG CTC TTC CGG AAG ATC AAC TGC	310
Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe Arg Lys Ile Asn Cys	
40 45 50	
AGA CTG TCC TAT TGC ATC TCA AGC CAG CTG GTG ATG CTG CTG GAG	355
Arg Leu Ser Tyr Cys Ile Ser Ser Gln Leu Val Met Leu Leu Glu	
55 60 65	
TGG TGG TCG GGC ACG GAA TGC ACC ATC TTC ACG GAC CCG CGC GCC	400
Trp Trp Ser Gly Thr Glu Cys Thr Ile Phe Thr Asp Pro Arg Ala	
70 75 80	
TAC CTC AAG TAT GGG AAG GAA AAT GCC ATC GTG GTT CTC AAC CAC	445
Tyr Leu Lys Tyr Gly Lys Glu Asn Ala Ile Val Val Leu Asn His	
85 90 95	
AAG TTT GAA ATT GAC TTT CTG TGT GGC TGG AGC CTG TCC GAA CGC	490
Lys Phe Glu Ile Asp Phe Leu Cys Gly Trp Ser Leu Ser Glu Arg	
100 105 110	
TTT GGG CTG TTA GGG GGC TCC AAG GTC CTG GCC AAG AAA GAG CTG	535
Phe Gly Leu Leu Gly Gly Ser Lys Val Leu Ala Lys Lys Glu Leu	
115 120 125	
GCC TAT GTC CCA ATT ATC GGC TGG ATG TGG TAC TTC ACC GAG ATG	580
Ala Tyr Val Pro Ile Ile Gly Trp Met Trp Tyr Phe Thr Glu Met	
130 135 140	
GTC TTC TGT TCG CGC AAG TGG GAG CAG GAT CGC AAG ACG GTT GCC	625
Val Phe Cys Ser Arg Lys Trp Glu Gln Asp Arg Lys Thr Val Ala	
145 150 155	
ACC AGT TTG CAG CAC CTC CGG GAC TAC CCC GAG AAG TAT TTT TTC	670
Thr Ser Leu Gln His Leu Arg Asp Tyr Pro Glu Lys Tyr Phe Phe	
160 165 170	
CTG ATT CAC TGT GAG GGC ACA CGG TTC ACG GAG AAG AAG CAT GAG	715
Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu Lys Lys His Glu	
175 180 185	
ATC AGC ATG CAG GTG GCC CGG GCC AAG GGG CTG CCT CGC CTC AAG	760
Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro Arg Leu Lys	
190 195 200	
CAT CAC CTG TTG CCA CGA ACC AAG GGC TTC GCC ATC ACC GTG AGG	805
His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr Val Arg	
205 210 215	
AGC TTG AGA AAT GTA GTT TCA GCT GTA TAT GAC TGT ACA CTC AAT	850
Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu Asn	
220 225 230	
TTC AGA AAT AAT GAA AAT CCA ACA CTG CTG GGA GTC CTA AAC GGA	895
Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	
235 240 245	
AAG AAA TAC CAT GCA GAT TTG TAT GTT AGG AGG ATC CCA CTG GAA	940
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu	
250 255 260	
GAC ATC CCT GAA GAC GAT GAC GAG TGC TCG GCC TGG CTG CAC AAG	985
Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys	
265 270 275	

Figure 11B

CTC TAC CAG GAG AAG GAT GCC TTT CAG GAG GAG TAC TAC AGG ACG	1030
Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr Tyr Arg Thr	
280 285 290	
GGC ACC TTC CCA GAG ACG CCC ATG GTG CCC CCC CGG CGG CCC TGG	1075
Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg Pro Trp	
295 300 305	
ACC CTC GTG AAC TGG CTG TTT TGG GCC TCG CTG GTG CTC TAC CCT	1120
Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr Pro	
310 315 320	
TTC TTC CAG TTC CTG GTC AGC ATG ATC AGG AGC GGG TCT TCC CTG	1165
Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu	
325 330 335	
ACG CTG GCC AGC TTC ATC CTC GTC TTC TTT GTG GCC TCC GTG GGA	1210
Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly	
340 345 350	
GTT CGA TGG ATG ATT GGT GTG ACG GAA ATT GAC AAG GGC TCT GCC	1255
Val Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala	
355 360 365	
TAC GGC AAC TCT GAC AGC AAG CAG AAA CTG AAT GAC TGA CTCAGGG	1301
Tyr Gly Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp ***	
370 375	
AGGTGTCACCATCCGAAGGGAACCTTGGGAACTGGTGGCCTCTGCATATCCTCCTTAGT	
GGGACACGGTGACAAAGGCTGGGTGAGCCCCTGCTGGGACGGCGGAAGTCACGACCTCT	
CCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTGTAAATCTTTTT	
TCCCCATGTGTTAGTGGCTTGGTTCTTTGTGCGAGTGTGTGAGAATGGCT	
GTGTGGTGAATGTGAACCTTGTCTGTGATCATAGAAAGGGTATTTAGGCTGAGGTTC	
GGGCAGGGCTGGGACCGAAGGGGACAAGTTCCCTTCATCCTTGGTGTGAGTTTC	
TGTAAACCTTGGTGCAGAGATAAAAGTGAAGTGTGAGATGACTAAATTAT	
GCCTCCAAGAAAAAAAAATTAAAGTGTCTGGTCAAAAAAAA	
1361	
1421	
1481	
1541	
1601	
1661	
1721	
1774	